

EXHIBIT IV



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.16 [Mar-25-2007]

Matrix BLOSUM62 gap open: 11 gap extension: 1

x_dropoff: 0 expect: 10.0000 wordsize: 3 Filter ☒ View option Mismatch-highlighting

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation

Sequence 1: lcl|seq_1

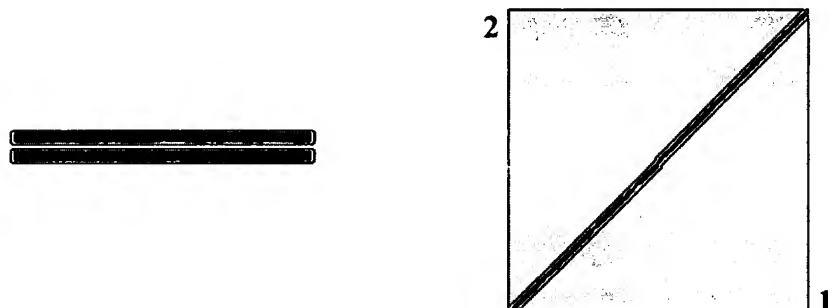
Length = 836 (1 .. 836)

Sequence 2: gi|14328879|gb|AAK02058.1|CUB domain containing protein 1 [Homo sapiens]

>gi|119585141|gb|EAW64737.1| CUB domain containing protein 1, isoform CRA_a [Homo sapiens]

>gi|119585142|gb|EAW64738.1| CUB domain containing protein 1, isoform CRA_a [Homo sapiens]

Length = 836 (1 .. 836)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 1556 bits (4030), Expect = 0.0
 Identities = 834/836 (99%), Positives = 836/836 (100%), Gaps = 0/836 (0%)

Query	1	MAGLNCGVSIALLGVLLLGAARLPRGAFAFEIALPRESNITVLIKLGTPDLLAKPCYIVI	60
Sbjct	1	60
Query	61	SKRHITMLSIKSGERIVFTFSCQSPENHFVIEIQKNIDCMGPCPFGEVQLQPSTSLPT	120
Sbjct	61	120
Query	121	LNRTFIWDVKAHKSIGLELQFSIPRLRQIGPGESCPDGVTHSISGRIDATVVRIGTFCSN	180
Sbjct	121	180
Query	181	GTVSRIKMQEGVKMALHLPWFHPRNVSGFSIANRSSIKRLCIIESVFEGEGSATLMSANY	240
Sbjct	181	240
Query	241	PEGFPEDELMTWQFVVPAPHLRASVSFLNFNLSNCERKEERVEYYIPGSTTNPEVFKLEDK	300
Sbjct	241	300
Query	301	QPGNMAGNFNLSLQGCDAQSPGILRLQFQVLVQHPQNESNKIYVVDLSNERAMSLTIE	360
Sbjct	301	360

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Query  361  PRPVKQSRKFVPGCFVCLESRTCSSNLTLTSGSKHKISFLCDDLTRLWMNVEKTISCTDH  420
Sbjct  361  .....  420

Query  421  RYCQRKSYSLQVPSDILHLPVELHDFSWKLLVPKDRLSLVLVPAQKLQQHTHEKPCNTSF  480
Sbjct  421  .....  480

Query  481  SYLVASAIPSQDLYFGSFCPGGSIKQIQVKQNISVTLRTFAPSFQRQEASRQGLTVSFIPY  540
Sbjct  481  .....Q.....  540

Query  541  FKEEGVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLTFFKERSGVVCQ  600
Sbjct  541  .....  600

Query  601  TGRAFMIIQEQRTRAEEIFSLDEDVLPKPSFHHHSFWVNISNCSPTSGKQLDLLFSVTLT  660
Sbjct  601  .....  660

Query  661  PRTVDLTVILIAAVGGGVLLLSALGLIICCVKKKKKKTKNGPAVGIYNGNINTEMPRQPK  720
Sbjct  661  .....  720

Query  721  KFQKGRKDNDSHVYAVIEDTMVYGHLLQDSSGSFLQPEVDTYRPFQGTMGVCPSPPTIC  780
Sbjct  721  .....  780

Query  781  SRAPTAKLATEEPPPRSPPESESEPYTFSHPNNGDVSSKDTDIPLLSTQEPMEPAE  836
Sbjct  781  .....N.....  836
```

CPU time: 0.04 user secs. 0.01 sys. secs 0.05 total secs.